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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Command line parameters:

-MODBL=frame+ p2n.model -DEV=soft -Q=Pending Patents AA Main:US-09-786-867-5

-DB=Pending Patents NA Main:US-09-786-867-1 -SUFFIX=pto -OUT=align5 1

-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS-bits -START=1 -END=-1

-MATRIX=blosum62 -TRANS=human40.cdi -LIST=1 -DOCALIGN=200 -THR SCORE=pct

-THR MAX=100 -THR MIN=0 -ALIGN=1 -MODB=LOCAL -OUTPMT=pto -NORM=ext

-HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO_XLPXY -NEG_SCORES=0

-LONGLOG -THREADS=1 -XGAPOD=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum
Maximum
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Maximum Match 100%
Listing first 1 summaries
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Ygapop 10.0
Fgapop 6.0
Delop 6.0
April 11, 2005, 13:27:16 ; Search time 18 Seconds (without alignments) 0.016 Million cell updates/sec
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891
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Copyright (c) 1993 - 2005 Compugen Ltd.
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31. (cgp2.6 (ptcodata I) (pma/(1819) PE (cmbs. seq; US-9) 7-18--18-7-1
34. (cgp2.6 (ptcodata I) (pma/(1819) PE (cmbs. seq; US-9) 7-18--18-7-1
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44. (cgp2.6 (ptcodata I) (pma/(1819) PE (cmbs. seq; US-9) 7-18--18-7-1
45. (cgp2.6 (ptcodata I) (pma/(1819) PE (cmbs. seq; US-9) 7-18--18-7-1
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48. (cgp2.6 (ptcodata I) (pma/(1819) PE (cmbs. seq; US-9) 7-18--18-7-1
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49. (cgp2.6 (ptcodata I) (pma/(1819) PE (cmbs. seq; US-9)
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468 CCTATCTCCCAGTCCTAGCTGCATGCATACAGACAGACCGCAACCTCAA, 527
            121 ProIleSerProSerProSerCysTrpHisHisThrThrThrAsnArgProGluProGln 140
                                          408 AIGGAGIGIGCATTACATTIGGAAAAAAAATGIGAATCAGTCACTACTGGAATTCCCTTCT 467
                                                      101 MetGluCysAlaLeuHisLeuGluLysAsnValAsnGlnSerLeuLeuGluPheProSer 120
                                                                                     348
                                                                                                                              61 HisGluGluArgGlnHisAlaGluLysLeuMetLysLeuGlnAsnGlnArgGlyGlyArg
                                                                                                                                                                                       ATCTTCCTTCAGGATATCAAGAAACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCA 407
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347

80 287 60 227 40

167

Search completed: April 11, 2005, 13:27:39
Job time : 19 secs

588

ATTITICGGICACCC 602

161 IlePheArgSerPro 165

528 CACCACCTTCTTCGACCCCGCCGGAGGAAGAGACCCCATTCTATACCAACACCTATTCTG

| HisHisLeuLeuArgProArgArgArgLysArgProHisSerIleProThrProIleLeu 160

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6/ptodata/1/pna/US6056_COMB. seq:US-09-786-867-1
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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141

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Result
No.
                    Query
Score Match Length DB ID
878
  98.5
  891 34
 US-09-786-867-1
                                                  SUMMARIES
                      Description
 Sequence 1, Appli
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## ALIGNMENTS

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RESULT 1
US-09-786-867-1
  Query Match:
DB:
                                    Percent Similarity:
Best Local Similarity:
                                                                            Score:
                                                                                            Alignment Scores: Pred. No.:
                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-786-867-1
                                                                                                                                                                                                   APPLICANT: MOROZ, Chaya
TITLE OF INVENTION: DNA SEQUENCE ENCODING ONCOFETAL FERRITIN PROTEIN
FILE REFERENCE: MOROZ=3
CURRENT APPLICATION NUMBER: US/09/786,867
CURRENT FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: PCT/L199/00485
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1998-09-11
RIUMBER OF SEQ ID NOS: 36
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
LENGTH: 891
TYPER. NUMBER

TURE: TURE DATE: 1988-09-11
SEQ ID NO 1
LENGTH: 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09786867
GENERAL INFORMATION:
0
878.00
99.39%
98.18%
98.54%
                Length:
Matches:
Conservative:
Mismatches:
Indels:
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US-09-786-867-5 (1-165) x US-09-786-867-1 (1-891)